AMENDMENTS TO THE CLAIMS

Claims 1 to 27 (cancelled)

Claim 28 (currently amended)

~~A fragment of a~~ An isolated nucleic acid specific to mycobacteria of M.tuberculosis complex having a nucleotide sequence selected from the group consisting of SEQ ID No: 1, SEQ ID No: 2, ~~and their complementary sequences~~ the complement of SEQ ID No: 1, and the complement of SEQ ID No: 2.

Claim 29 (currently amended)

~~A fragment of a~~ An isolated nucleic acid specific to mycobacteria of M.tuberculosis complex having a nucleotide sequence selected from the group consisting of SEQ ID No: 1 and ~~its~~ the ~~complementary sequence~~ complement of SEQ ID No: 1.

Claim 30 (currently amended)

~~A fragment of a~~ An isolated nucleic acid specific to mycobacteria of M.tuberculosis complex which ~~fragment~~ mycobacteria is different from BCG, ~~and~~ whereas said nucleic acid has a nucleotide sequence selected from the group consisting of SEQ ID No: 2 and ~~its~~ the ~~complementary sequence~~ complement of SEQ ID No: 2.

Claim 31 (previously presented)

A cloning or expression vector containing a nucleic acid sequence of claim 28.

Claim 32 (previously presented)

A vector of claim 31 which is a plasmid selected from the group consisting of pRegX3Bc1 and pRegX3Mt1deposited at CNCM under Nos. I-1765 and I-1766, respectively.

Claim 33 (currently amended)

A nucleotide probe or nucleotide primer that hybridizes at 68°C in a 5xSSC hybridization buffer ~~under high stringency conditions~~ with one of the sequences ~~of claim 28, its~~ selected from the group consisting of SEQ ID No: 1, SEQ ID No: 2, the complement of SEQ ID No: 1, and the complement of SEQ ID No: 2, their corresponding RNA sequences or ~~its~~ their corresponding gene, and that contains a maximum of 21 base pairs.

Claim 34 (currently amended)

A nucleotide probe of claim 33 comprising 24 consecutive nucleotides selected from ~~the sequences~~ a sequence ~~of claim 28~~ selected from the group consisting of SEQ ID No:1, SEQ ID No: 2, the complement of SEQ ID No: 1, and the complement of SEQ ID No: 2.

Claim 35 (currently amended)

A nucleotide probe of claim 33 comprising sequence SEQ ID No: 1 or ~~its complementary strand~~ the complement of SEQ ID No: 1.

Claim 36 (previously presented)

A nucleotide probe of claim 33 comprising two successive sequences SEQ ID No: 1 followed by a sequence SEQ ID No: 2.

Claim 37 (currently amended)

A nucleotide probe for detection of specific sequences of nucleic acids of M.tuberculosis complex other than BCG wherein said probe ~~comprising~~ comprises a ~~sequence of the~~ region of sequence SEQ ID No: 2 comprising the GAG codon in positions 40 to 42 or ~~its~~ the ~~complementary strand~~ complement of said region.

Claim 38 (currently amended)

A nucleotide probe of claim 37 comprising a sequence composed of ~~9 base paris upstream and 9 base paris downstream of the GAG codon~~ nucleotides in positions ~~40 to 42~~ 31 to 51 of SEQ ID No: 2 or ~~its complementary strand~~ the complement of said sequence.

Claim 39 (currently amended)

A nucleotide probe of claim 37 comprising a sequence composed of ~~9 base paris upstream and 9 base paris downstream of the GAG codon~~ nucleotides in positions ~~40 to 42~~ 31 to 51 of SEQ ID NO: 2.

Claim 40 (currently amended)

A nucleotide probe of claim 37 comprising the sequence SEQ ID No: 2 or ~~its~~ the ~~complementary strand~~ complement of SEQ ID No: 2.

Claim 41 (previously presented)

A nucleotide probe of claim 33 labelled by dioxygenin.

Claim 42 (currently amended)

A nucleotide primer pair for amplification of a specific nucleotide sequence of mycobacteria of M. tuberculosis complex, ~~said pair comprising~~ wherein one primer comprises the nucleotide sequence of sequences adjacent to the senX3-regX3 region in the 3' of seX3 region and the other primer comprises the nucleotide sequence of sequences adjacent to the senX3-regX3 region in the ~~and~~ 5' of regX3 regions.

Claim 43 (previously presented)

A nucleotide primer of claim 42 comprising 19 nucleotides.

Claim 44 (previously presented)

A nucleotide primer pair of claim 42 comprising the pair of primers 5'GCGCGAGAGCCCGAACTGC3' (SEQ ID No: 4) and 5'GCGCAGCAGAAACGTCAGC3' (SEQ ID No: 5).

Claims 45 and 46 (cancelled)

Claim 47 (currently amended)

A method of detecting a mycobacteria stain of M. tuberculosis complex in a biological sample comprising (1) contacting the biological sample to a pair of primers ~~of claim 42~~ wherein one primer comprises the nucleotide sequence of sequences adjacent to the senX3-regX3 region in the 3' of senX3 region and the other primer comprises the nucleotide sequence of sequences adjacent to the senX3-regX3 region in the 5' of regX3 region under conditions to effect hybridization of the primers to the specific nucleic acids of mycobacteria strains of M. tuberculosis complex, (2) effecting amplification of the said nucleic acids, (3) contacting the biological sample with a nucleotide probe ~~of claim 33~~ that hybridizes at 68°C in a 5xSSC hybridization buffer with one of the sequences selected from the group consisting of SEQ ID No: 1, SEQ ID No: 2, the complement of SEQ ID No: 1, and the complement of SEQ ID No: 2, their corresponding RNA sequences or their corresponding gene, and that contains a maximum of 21 base pairs under conditions for formation of hybridization complexes between the said probe and

amplified sequences of nucleic acids and (4) detecting if any hybridization complexes are present, which complexes indicate the presence of a mycobacteria strain of M. tuberculosis.

Claim 48 (currently amended)

The method of claim 47 wherein the nucleotide probe ~~is that of claim 35~~ comprises sequence SEQ ID No: 1 or the complement of SEQ ID No: 1.

Claim 49 (currently amended)

The method of claim 47 wherein the nucleotide probe ~~is that of claim 37~~ comprises a region of SEQ ID No: 2 comprising the GAG codon in positions 40 to 42 or the complement of said region.

Claim 50 (previously presented)

The method of claim 49 effected upon immunodeficient humans to differentiate an infection by BCG from an infection by a virulent mycobacterium of M. tuberculosis complex.

Claim 51 (previously presented)

The method of claim 50 wherein the human is infected with HIV.

Claim 52 (previously presented)

A method of identifying groups of mycobacteria belonging to a M. tuberculosis complex comprising (1) contacting the DNA of previously extracted strains of the M. tuberculosis complex with a pair of primers of claims 35 and 42 under conditions permitting a specific hybridization of the primers with one of the sequences of claim 28 to obtain amplification products and (2) measuring the length of the amplification products obtained.

Claim 53 (currently amended)

The method of claim 52 wherein the pair of primers are

5'GCGCGAGAGCCCGAACTGC3' (SEQ ID No: 4) and

5'GCGCAGCAGAAACGTCAGC3' (SEQ ID No: 5);

Claim 54 (currently amended)

A kit for in vitro identification of strains of mycobacteria of the M. tuberculosis complex in a ~~biologicalo~~ biological sample comprising (1) a primer pair for amplification of a specific nucleotide sequence of mycobacteria of M. tuberculosis complex, ~~said pair~~ one primer comprising the nucleotide sequence of sequences adjacent to the senX3-regX3 region in the 3' of seX3 ~~and~~ region and the other primer comprising the nucleotide sequence of sequences adjacent to the senX3-regX3 region in the 5' of regX3 regions.

Claim 55 (currently amended)

A method of detection and of differential diagnosis of BCG and the members of M. tuberculosis complex in a biological complex comprising:

(1) contacting the biological sample to a nucleotide primer pair for amplification of a specific nucleotide sequence of mycobacteria of M. tuberculosis complex, ~~said pair~~ one primer comprising the nucleotide sequence of sequences adjacent to the senX3-regX~~e~~3 region in the 3' of seX3 ~~and~~ region and the other primer comprising the nucleotide sequence of sequences adjacent to the senX3-regX3 region in the 5' ~~or~~ of regX3 regions under conditions to effect hybridization of the primers to the specific nucleic acids of mycobacteria strains of M. tuberculosis complex;

(2) effecting amplification of the said nucleic acids;

(3) contacting the biological sample with a nucleotide probe of two successive sequences SEQ ID No: 1 followed by a sequence SEQ ID No: 2 under conditions for formation of hybridization complexes between the said probe and amplified sequences of nucleic acids; and

(4) detecting any first hybridization complexes present; and

(5) determining if said first hybridization complexes are also capable of forming second hybridization complexes with a nucleotide probe for detection of specific sequences of nucleic acids of M. tuberculosis complex other than BCG comprising a sequence of the region of sequence SEQ ID No: 2 comprising the GAG codon in positions 40 to 42 or its complementary strand, the presence of said second hybridization complexes being indicative of the presence of a M. tuberculosis strain different from BCG.